

NM\_198185 ACCESSION:NM\_198185 NID: gi 38044105 ref NM\_198185.1  
Homo sapiens oviductin protease (OVTN), mRNA  
Length = 1695

Score = 619 bits (1580), Expect = e-175  
Identities = 300/302 (99%), Positives = 300/302 (99%), Gaps = 0/302 (0%)  
Frame = +1

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Query: 303 GN 304  
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Sbjct: 901 GN 906



Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

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Show:

☐ 1: NM\_198185. Homo sapiens ovid...[gi:38044105]

Links

LOCUS NM\_198185 1695 bp mRNA linear PRI 30-OCT-2003

DEFINITION Homo sapiens oviductin protease (OVTN), mRNA.

ACCESSION NM\_198185

VERSION NM\_198185.1 GI:38044105

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Puente,X.S., Sanchez,L.M., Overall,C.M. and Lopez-Otin,C.

TITLE Human and mouse proteases: a comparative genomic approach

JOURNAL Nat. Rev. Genet. 4 (7), 544-558 (2003)

MEDLINE 22722134

PUBMED 12838346

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from BN000120.1.

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## ORIGIN

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//

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Nov 3 2003 07:26:36

Homo sapiens. Human CVSP14 full length cDNA. PA:CORVAS INT INC.

PN:WO200277263-A2. gsn

Length = 1035

Score = 628 bits (1603), Expect = e-179

Identities = 305/306 (99%), Positives = 306/306 (100%), Gaps = 0/306 (0%)

Frame = +1

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Presentation:

Basic

Image:

Small

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## PUBLISHED INTERNATIONAL APPLICATION

- (11) **WO 02/077263** (13) A2  
 (21) PCT/US02/09039  
 (22) **20 March 2002 (20.03.2002)**  
 (25) ENG (26) ENG  
 (31) 60/278,166 (32) 22 March 2001 (22.03.2001) US  
 (43) 03 October 2002 (03.10.2002)  
 (51)<sup>7</sup> C12Q  
 (54) NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE  
 CVSP14, THE ENCODED POLYPEPTIDES AND METHODS  
 BASED THEREON  
 (61) US 60/278,166 (CIP)  
 Filed on 22 March 2001 (22.03.2001)  
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 (81)  
 AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
 CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,  
 GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
 LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
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 TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW  
 (84)  
 ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM,  
 ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
 European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
 IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,  
 GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

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Published *without international search report and to be republished upon receipt of that report*

Declaration under Rule 4.17 *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations*  
 AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)  
*as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for the following designations* AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

No Image Available.

## Abstract

Provided herein are polypeptides designated CVSP14 polypeptides that exhibit protease activity as a single chain or as an activated two chain form. Methods using the polypeptides to identify compounds that modulate the protease activity thereof are provided. The polypeptides also serve as tumor markers.



Presentation:

Basic

Image:

Small

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1 of 2

Homo sapiens. Human protease PRTS-20 cDNA sequence. PA:INCYTE GENOMICS INC.  
PN:W0200198468-A2. gsn  
Length = 1262

Score = 628 bits (1603), Expect = e-179  
Identities = 305/306 (99%), Positives = 305/306 (99%), Gaps = 0/306 (0%)  
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Français

1 of 1

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## PUBLISHED INTERNATIONAL APPLICATION

- (11) **WO 01/98468** (13) A2
- (21) PCT/US01/19178
- (22) **13 June 2001 (13.06.2001)**
- (25) ENG (26) ENG
- (31) 60/212,336 (32) 16 June 2000 (16.06.2000) US
- (31) 60/213,955 (32) 22 June 2000 (22.06.2000) US
- (31) 60/215,396 (32) 29 June 2000 (29.06.2000) US
- (31) 60/216,821 (32) 07 July 2000 (07.07.2000) US
- (31) 60/218,946 (32) 14 July 2000 (14.07.2000) US
- (43) 27 December 2001 (27.12.2001)
- (51)<sup>7</sup> C12N 9/00
- (54) PROTEASES
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(81)

AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
 CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE,  
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 NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,  
 UA, UG, US, UZ, VN, YU, ZA, ZW

(84)

ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG,  
 ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
 European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
 IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,  
 GA, GN, GW, ML, MR, NE, SN, TD, TG)

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Published *without international search report and to be republished  
 upon receipt of that report*

No Image Available.

## Abstract

The invention provides human proteases (PRTS) and polynucleotides which identify and encode PRTS. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of PRTS.



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characterize the protein. A starting material that can only be used to produce a final product does not have a substantial asserted utility in those instances where the final product is not supported by a specific and substantial utility. In this case none of the proteins that are to be produced as final products resulting from processes involving the claimed cDNA have asserted or identified specific and substantial utilities. The research contemplated by Applicants to characterize potential protein products, especially their biological activities, does not constitute a specific and substantial utility. Identifying and studying the properties of the protein itself or the mechanisms in which the protein is involved does not define a "real world" context of use. Note, because the claimed invention is not supported by a specific and substantial asserted utility for the reasons set forth above, credibility has not been assessed. Neither the specification as filed nor any art of record discloses or suggests any property or activity for the cDNA compounds such that another non-asserted utility would be well established for the compounds.

Claim 1 is also rejected under 35 U.S.C. § 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art would not know how to use the claimed invention.

**Example 10: DNA Fragment encoding a Full Open Reading Frame (ORF)**

**Specification:** The specification discloses that a cDNA library was prepared from human kidney epithelial cells and 5000 members of this library were

sequenced and open reading frames were identified. The specification discloses a Table that indicates that one member of the library having SEQ ID NO: 2 has a high level of homology to a DNA ligase. The specification teaches that this complete ORF (SEQ ID NO: 2) encodes SEQ ID NO: 3. An alignment of SEQ ID NO: 3 with known amino acid sequences of DNA ligases indicates that there is a high level of sequence conservation between the various known ligases. The overall level of sequence similarity between SEQ ID NO: 3 and the consensus sequence of the known DNA ligases that are presented in the specification reveals a similarity score of 95%. A search of the prior art confirms that SEQ ID NO: 2 has high homology to DNA Ligase encoding nucleic acids and that the next highest level of homology is to alpha-actin. However, the latter homology is only 50%. Based on the sequence homologies, the specification asserts that SEQ ID NO: 2 encodes a DNA ligase.

**Claim 1:** An isolated and purified nucleic acid comprising SEQ ID NO: 2.

**Analysis:** The following analysis includes the questions that need to be asked according to the guidelines and the answers to those questions based on the above facts:

1) Based on the record, is there a "well established utility" for the claimed invention? Based upon applicant's disclosure and the results of the PTO search, there is no reason to doubt the assertion that SEQ ID NO: 2 encodes a DNA ligase. Further, DNA ligases have a well-established use in the molecular biology art based on this class of protein's ability to ligate DNA. Consequently the answer to the question is yes.

Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed. In order to determine whether the claimed invention has a well-established utility the examiner must determine that the invention has a specific, substantial and credible utility that would have been readily apparent to one of skill in the art. In this case SEQ ID NO: 2 was shown to encode a DNA ligase that the artisan would have recognized as having a specific, substantial and credible utility based on its enzymatic activity.

Thus, the conclusion reached from this analysis is that a 35 U.S.C. § 101 rejection and a 35 U.S.C. § 112, first paragraph, utility rejection should not be made.

**Example 11: Animals with Uncharacterized Human Genes**

**Specification:** Kidney cells from a patient with Polycystic Kidney (PCK) Disease have been used to make a cDNA library. From this library 8000 nucleotide "fragments" have been sequenced but not yet used to express proteins in a transformed host cell nor have they been characterized in any other way. The 50 longest fragments, SEQ ID NO: 1-50, respectively, have been used to make transgenic mice. None of the 50 lines of mice have developed Polycystic Kidney Disease to date. The asserted utility is the use of the mice to research human genes from diseased human kidneys. The disease is inheritable, but chromosomal loci have not yet been identified. Neither the absence or presence of a specific protein has been identified with the disease condition.

Query= SEQ ID NO:1  
(921 letters)

Sequences producing significant alignments:

|  | Score<br>(bits) | E<br>Value |
|--|-----------------|------------|
|--|-----------------|------------|

|                     |            |       |
|---------------------|------------|-------|
| AC104237.2.1.164732 | <u>391</u> | e-106 |
|---------------------|------------|-------|

>AC104237.2.1.164732  
Length = 164732

Score = 391 bits (197), Expect = e-106  
Identities = 200/201 (99%)  
Strand = Plus / Plus

|              |  |       |
|--------------|--|-------|
| Query: 721   | cagggagattcaggaggttcactcatgtgccggaataagaaaggggcctggactctggct | 780   |
|              |  |       |
| Sbjct: 51293 | cagggagattcaggaggttcactcatgtgccggaataagaaaggggcctggactctggct | 51352 |

|              |  |       |
|--------------|--|-------|
| Query: 781   | ggtgtgacttcctgggggttgggctgtggtcgaggctggagaaacaatgtgaggaaaagt | 840   |
|              |  |       |
| Sbjct: 51353 | ggtgtgacttcctgggggttgggctgtggtcgaggctggagaaacaatgtgaggaaaagt | 51412 |

|              |  |       |
|--------------|--|-------|
| Query: 841   | gatcaaggatcccctgggatcttcacagacattagtaaagtgctttcctggatccacgaa | 900   |
|              |  |       |
| Sbjct: 51413 | gatcaaggatcccctgggatcttcacagacattagtaaagtgctttcctggatccacgaa | 51472 |

|              |                       |       |
|--------------|-----------------------|-------|
| Query: 901   | cacatccaaactggtaactaa | 921   |
|              |                       |       |
| Sbjct: 51473 | cacatccaaactggtaactaa | 51493 |

Score = 349 bits (176), Expect = 1e-93  
Identities = 176/176 (100%)  
Strand = Plus / Plus

|              |  |       |
|--------------|--|-------|
| Query: 301   | agaaacattgtgtctactttgaatgttactgctggagagtatgacttaagccagacagac | 360   |
|              |  |       |
| Sbjct: 49450 | agaaacattgtgtctactttgaatgttactgctggagagtatgacttaagccagacagac | 49509 |

|              |   |       |
|--------------|---|-------|
| Query: 361   | ccaggagagcaaaactctcactattgaaactgtcatcatatccacatttctccaccaag | 420   |
|              |   |       |
| Sbjct: 49510 | ccaggagagcaaaactctcactattgaaactgtcatcatatccacatttctccaccaag | 49569 |

|              |  |       |
|--------------|--|-------|
| Query: 421   | aaaccaatggactatgatattgcccttttgaagatggctggagccttccaatttgg | 476   |
|              |  |       |
| Sbjct: 49570 | aaaccaatggactatgatattgcccttttgaagatggctggagccttccaatttgg | 49625 |

Score = 308 bits (155), Expect = 5e-81  
Identities = 155/155 (100%)  
Strand = Plus / Plus

Query: 570 aggtggcgctcctctcacaaagtcttgcaggaagtgaatctgcctattttgacctgggaaga 629  
|||||  
Sbjct: 50304 aggtggcgctcctctcacaaagtcttgcaggaagtgaatctgcctattttgacctgggaaga 50363

Query: 630 gtgtgtggcagctctgttaacactaaagaggcccatcagtgggaagacctttctttgcac 689  
|||||  
Sbjct: 50364 gtgtgtggcagctctgttaacactaaagaggcccatcagtgggaagacctttctttgcac 50423

Query: 690 aggttttcctgatggaggaggagagacgcatgtcagg 724  
|||||  
Sbjct: 50424 aggttttcctgatggaggaggagagacgcatgtcagg 50458

Score = 226 bits (114), Expect = 2e-56  
Identities = 114/114 (100%)  
Strand = Plus / Plus

Query: 99 agctcccagttgtgggcagagtctgggtaagggtacagccttggaattattttaacatttt 158  
|||||  
Sbjct: 47105 agctcccagttgtgggcagagtctgggtaagggtacagccttggaattattttaacatttt 47164

Query: 159 cagtcgcattcttggaggaagccaagtggagaaggggttcctatccctggcaggt 212  
|||||  
Sbjct: 47165 cagtcgcattcttggaggaagccaagtggagaaggggttcctatccctggcaggt 47218

Score = 197 bits (99), Expect = 1e-47  
Identities = 99/99 (100%)  
Strand = Plus / Plus

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|||||  
Sbjct: 49969 ggccactttgtggggcccatatgtcttccagagctgcgggagcaatttgaggctgggtttt 50028

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|||||  
Sbjct: 50029 atttgtacaactgcaggctggggccgcttaactgaaggt 50067

Score = 191 bits (96), Expect = 9e-46  
Identities = 98/100 (98%)  
Strand = Plus / Plus

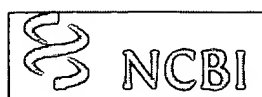
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Query: 61 tttgaacraggtaaactctgcarctctttcgctccccaag 100  
|||||  
Sbjct: 45435 tttgaacraggtaaactctgcaactctttcgctccccaag 45474

Score = 187 bits (94), Expect = 1e-44  
Identities = 94/94 (100%)  
Strand = Plus / Plus

Query: 209 aggtatctctgaaacaaaggcagaagcatatttgtggaggaagcatcgtctcaccacagt 268  
|||||  
Sbjct: 47990 aggtatctctgaaacaaaggcagaagcatatttgtggaggaagcatcgtctcaccacagt 48049

Query: 269 ggggtgatcacggcggtcactgcattgcaaacag 302  
|||||  
Sbjct: 48050 ggggtgatcacggcggtcactgcattgcaaacag 48083



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LOCUS AC104237 164732 bp DNA linear PRI 30-APR-2002

DEFINITION Homo sapiens chromosome 11, clone RP11-35J10, complete sequence.

ACCESSION AC104237

VERSION AC104237.2 GI:20128277

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 164732)

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TITLE Homo sapiens chromosome 11, clone RP11-35J10

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 164732)

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